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Figure 1

### Cloning of the endothelial cell tropic and leukotropic clinical isolate VR1814 as FIX-BAC

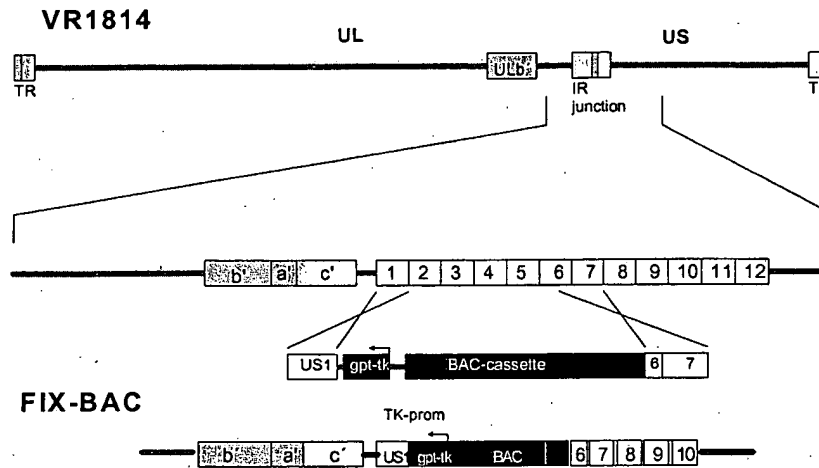


Fig. 1 Construction of FIX-BAC. A gpt-tk-BAC cassette was introduced into the US2-6 region of the parental virus VR1814 as described in patent application PCT/EP02/01867 (WO 02/066629).

Figure 2

**RVFIX virus mutants**

RVFIX $\Delta$ ULb'	nt 175662-189347
RVFIX $\Delta$ UL132-128	nt 174857-176865
RVFIX $\Delta$ UL133-148	nt 177896-189347
RVFIX $\Delta$ UL132-130	nt 175662-177743
RVFIX $\Delta$ UL131K	nt 176377-176776
RVFIX $\Delta$ UL130	nt 175662-176314
RVFIX $\Delta$ UL128K	nt 174953-175387
RVFIX $\Delta$ UL132K	nt 177076-177752
RVFIX $\Delta$ UL148	nt 177896-178644
RVFIX $\Delta$ UL146-147	nt 179069-179966
RVFIX $\Delta$ UL127	nt 174467-174770

**Deletion according to (Chee, Bankier et al., 1990)**

Fig. 2 List of RVFIX virus mutants and determination of the mutation (kanamycin cassette insertion) according to annotation by {Chee, Bankier, et al. 1990 269 /id}

Figure 3 shows an agarose gel and Southern Blot of RVFIX and RVFIX mutant viruses.

Figure 3

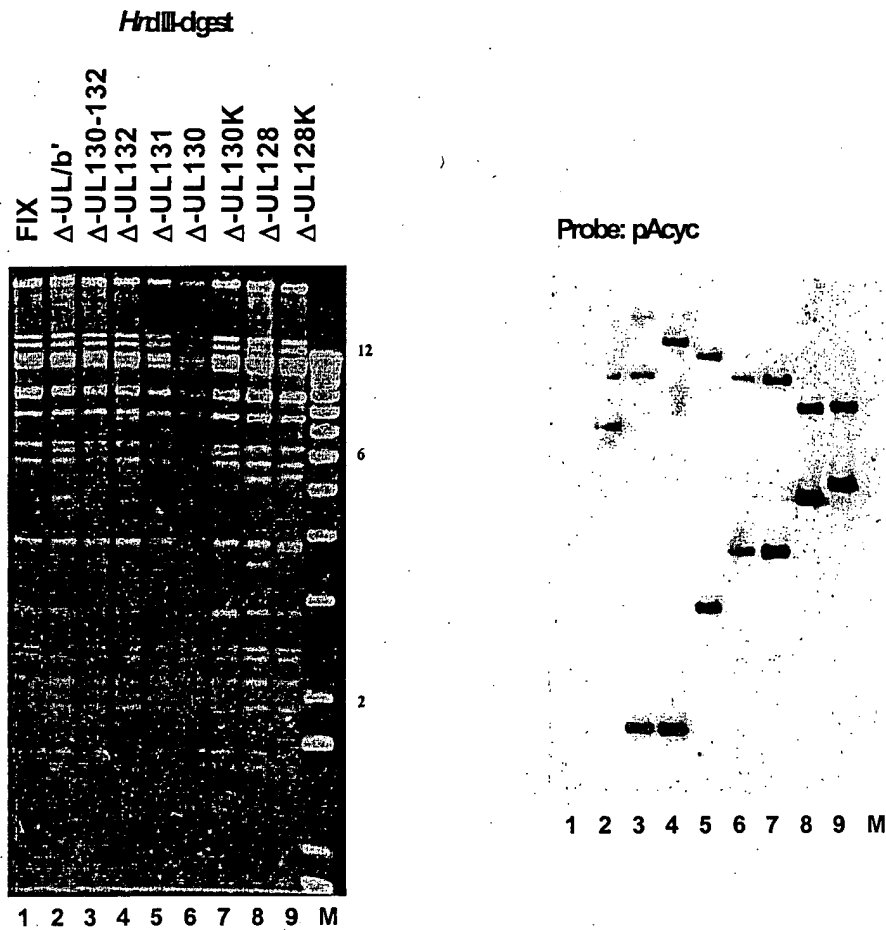


Fig.3 DNA derived from individually grown FIX-BAC clones (lane 1) or FIX-BAC mutant clones  $\Delta$ ULb',  $\Delta$ UL130-132,  $\Delta$ UL132,  $\Delta$ UL131,  $\Delta$ UL130,  $\Delta$ UL130K,  $\Delta$ UL128 and  $\Delta$ UL128K (lanes 2-9) was digested with *Hind*III and run on a 0.5% agarose gel.

Figure 4

A

FIX 176834-GTCTGCAACATGCGGCTGTGTGCGGTGTGGCTGTCTGTTTGTCTGTGCGCCGTGGTGTCTG  
 RACE\_95\_3 GTCTGCAACATGCGGCTGTCTGCGGTGTGGCTGTCTGTTTGTCTGTGCGCCGTGGTGTCTG  
 RACE\_95\_8 GTCTGCAACATGCGGCTGTGTGCGGTGTGGCTGTCTGTTTGTCTGTGCGCCGTGGTGTCTG  
 RACE\_95\_11 GTCTGCAACATGCGGCTGTGTGCGGTGTGGCTGTCTGTTTGTCTGTGCGCCGTGGTGTCTG

FIX GGTCAAGTCCAGCGGGAGACCGCAGAAAAA--CGATTATTACCGAGTACCGCATTACT  
 RACE\_95\_3 GGTCAAGTCCAGCGGGAGACCGCAGAAAAA--CGATTATTACCGAGTACCGCATTACT  
 RACE\_95\_8 GGTCAAGTCCAGCGGGAGACCGCAGAAAAA--CGATTATTACCGAGTACCGCATTACT  
 RACE\_95\_11 GGTCAAGTCCAGCGGGAGACCGCAGAAAAA--CGATTATTACCGAGTACCGCATTACT

FIX GGGACGCGTGCTCTCGCGCGCTGCCTGACCAAACCCGTTACAAGTATGTGGAACAGCTCG  
 RACE\_95\_3 GGGACGCGTGCTCTCGCGCGCTGCCTGACCAAACCCGTTACAAGTATGTGGAACAGCTCG  
 RACE\_95\_8 GGGACGCGTGCTCTCGCGCGCTGCCTGACCAAACCCGTTACAAGTATGTGGAACAGCTCG  
 RACE\_95\_11 GGGACGCGTGCTCTCGCGCGCTGCCTGACCAAACCCGTTACAAGTATGTGGAACAGCTCG

FIX TGGACCTCACGTTGAACTACCACTACGATGCGAGCCACGGCTTGGACAACCTTTGACGTGC  
 RACE\_95\_3 TGGACCTCACGTTGAACTACCACTACGATGCGAGCCACGGCTTGGACAACCTTTGACGTGC  
 RACE\_95\_8 TGGACCTCACGTTGAACTACCACTACGATGCGAGCCACGGCTTGGACAACCTTTGACGTGC  
 RACE\_95\_11 TGGACCTCACGTTGAACTACCACTACGATGCGAGCCACGGCTTGGACAACCTTTGACGTGC

FIX TCAAGAGGTGAGGGTACGCGCTAAAGGTGTATGACAACGGGAAGGTAAGGGCGAACGGGT  
 RACE\_95\_3 TCAAGAG-----  
 RACE\_95\_8 TCAAGAGGTGAGGGTACGCGCTAAAGGTGTATGACAACGGGAAGGTAAGGGCGAACGGGT  
 RACE\_95\_11 TCAAGAG-----

FIX AACGGGTAGGTAACCGCATGGGGTGTGAAATGACGTTTCGGAACCTGTGCTTGCAATCA  
 RACE\_95\_3 -----AATCA  
 RACE\_95\_8 AACGGGTAGGTAACCGCATGGGGTGTGAAATGACGTTTCGGAACCTGTGCTTGCAATCA  
 RACE\_95\_11 -----AATCA

FIX ACGTGACCGAGGTGTGCTGCTCATCAGCGACTTTAGACGTCAGAACCCTCGCGGGCGGCA  
 RACE\_95\_3 ACGTGACCGAGGTGTGCTGCTCATCAGCGACTTTATACGTCAGAACCCTCGCGGGCGGCA  
 RACE\_95\_8 ACGTGACCGAGGTGTGCTGCTCATCAGCGACTTTAGACGTCAGAACCCTCGCGGGCGGCA  
 RACE\_95\_11 ACGTGACCGAGGTGTGCTGCTCATCAGCGACTTTAGACGTCAGAACCCTCGCGGGCGGCA

FIX CCAACAAAAGGACCACGTTCAACGCCGCCGGTTCGCTGGCGCCTCACGCCCCGAGCCTCG  
 RACE\_95\_3 CCAACAAAAGGACCACGTTCAACGCCGCCGGTTCGCTGGCGCCTCACGCCCCGAGCCTCG  
 RACE\_95\_8 CCAACAAAAGGACCACGTTCAACGCCGCCGGTTCGCTGGCGCCTCACGCCCCGAGCCTCG  
 RACE\_95\_11 CCAACAAAAGGACCACGTTCAACGCCGCCGGTTCGCTGGCGCCTCACGCCCCGAGCCTCG

FIX AGTTCAGCGTGCGGCTCTTTGCCAACTAGCCTGCGTCA-176346  
 RACE\_95\_3 AGTTCAGCGTGCGGCTCTTTGCCAACTAGCCTGCGTCA  
 RACE\_95\_8 AGTTCAGCGTGCGGCTCTTTGCCAACTAGCCTGCGTCA  
 RACE\_95\_11 AGTTCAGCGTGCGGCTCTTTGCCAACTAGCCTGCGTCA

B

FIX 175631-CCGCGCGTCATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTATTG  
 RACE\_95\_3 CCGTGCGTCATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTATTG  
 RACE\_95\_8 CCGCGCGTCATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTATTG  
 RACE\_95\_13 CCGCGCGTCATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTATTG

FIX7 GGTACAGCCGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCAAC  
 RACE\_95\_3 GGTACAGCCGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCAAC  
 RACE\_95\_8 GGTACAGCCGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCAAC  
 RACE\_95\_11 GGTACAGCCGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCAAC

FIX CACCCGCCGAACGCTGTTACGATTTCAAATGTGCAATCGCTTCACCGTCGCGTACGTA  
 RACE\_95\_3 CACCCGCCGAACGCTGTTACGATTTCAAATGTGCAATCGCTTCACCGTCGCGTACGTA  
 RACE\_95\_8 CACCCGCCGAACGCTGTTACGATTTCAAATGTGCAATCGCTTCACCGTCGCGTACGTA  
 RACE\_95\_11 CACCCGCCGAACGCTGTTACGATTTCAAATGTGCAATCGCTTCACCGTCGC-----

FIX TTTTATGATTGTCTGCGTTCTGTGGTGGCTCTGGATTGTCTCTCGACGTTTCTGATAG  
 RACE\_95\_3 TTTTCATGATTGTCTGCGTTCTGTGGTGGCTCTGGATCTGTCTCTCGACGTTTCTGATAG  
 RACE\_95\_8 TTTTCATGATTGTCTGCGTTCTGTGGTGGCTCTGGATCTGTCTCTCGACGTTTCTGATAG  
 RACE\_95\_11 -----

FIX CCATGTTCCATCGACGATCCTCGGGAATGCCAGAGTAGATTTTCATGAATCCACAGGCTG  
 RACE\_95\_3 CCATGTTCCATCGACGATCCTCGGGAATGCCAGAGTAGATTTTCATGAATCCACAGGCTG  
 RACE\_95\_8 CCATGTTCCATCGACGATCCTCGGGAATGCCAGAGTAGATTTTCATGAATCCACAGGCTG  
 RACE\_95\_11 -----GCTG

FIX CGGTGTCCGGACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTGCGGGGATC  
 RACE\_95\_3 CGGTGTCCGGACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTGCGGGGATC  
 RACE\_95\_8 CGGTGTCCGGACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTGCGGGGATC  
 RACE\_95\_11 CGGTGTCCGGACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTGCGGGGATC

FIX GTCACCACCATGACCCATTTCATTGACACGCCAGGTCGTACACAACAACTGACGAGCTGC  
 RACE\_95\_3 GTCACCACCATGACCCATTTCATTGACACGCCAGGTCGTACACAACAACTGACGAACTGC  
 RACE\_95\_8 GTCACCACCATGACCCATTTCATTGACACGCCAGGTCGTACACAACAACTGACGAGCTGC  
 RACE\_95\_11 GTCACCACCATGACCCATTTCATTGACACGCCAGGTCGTACACAACAACTGACGAGCTGC

FIX AACTACAATCCGTAAGTCTCTTCCTCGAGGGCCTTACAGCCTATGGGAAAGTAAGACAGA  
 RACE\_95\_3 AACTACAATCC-----  
 RACE\_95\_8 AACTACAATCC-----  
 RACE\_95\_11 AACTACAATCT-----

FIX GGGACAAAACATCATTAATAAAAAAGTCTAATTTACAGTTTTGTACCCCCCTTCCCCTC  
 RACE\_95\_3 -----  
 RACE\_95\_8 -----  
 RACE\_95\_11 -----

FIX CGTGTGTAGGTTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAACGACA  
 RACE\_95\_3 -----GTTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAACGACA  
 RACE\_95\_8 -----GTTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAACGACA  
 RACE\_95\_11 -----GTTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAACGACA

FIX AGGCGCAGTACCTGCTGGGCGCCGCTGGCAGCGTTCCCTATCGATGGATCAACCTGGAAT  
 RACE\_95\_3 AGGCGCAGTACCTGCTGGGCGCCGCTGGCAGCGTTCCCTATCGATGGATCAACCTGGAAT  
 RACE\_95\_8 AGGCGCAGTACCTGCTGGGCGCCGCTGGCAGCGTTCCCTATCGATGGATCAACCTGGAAT  
 RACE\_95\_11 AGGCGCAGTACCTGCTGGGCGCCGCTGGCAGCGTTCCCTATCGATGGATCAACCTGGAAT

FIX ACGACAAGATAACCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAACACA  
 RACE\_95\_3 ACGACAAGATAACCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAACACA  
 RACE\_95\_8 ACGACAAGATAACCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAACACA  
 RACE\_95\_11 ACGACAAGATAACCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAATACA

FIX AACGGCTGGATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAA-174887  
 RACE\_95\_3 AACGGCTGGATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAA----  
 RACE\_95\_8 AACGGCTGGATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAA----  
 RACE\_95\_11 AACGGCTGGATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAA----

C

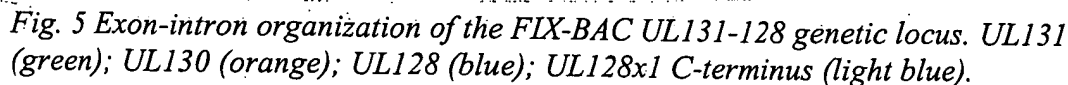
FIX 174892-CGCTAAAATGGGCTATATGCTGCAGTGAATAATAAAATGTGTGTTGTCCGA-174841

```

RACE_95_3  -- CGCTAAATGGGCTATATGCTGCAGTGAATAATAAAATGTGTGTTGTCCGCAAAAAAAAA --
RACE_95_8  -- CGCTAAATGGGCTATATGCTGCAGT AATAATAAAATGTGTGTTGTCCAAAAAAAAAA --
RACE_95_11 -- CGCTAAATGGGCTATATGCTGCAGTGAATAATAAAATGTGTGTTGTCCAAAAAAAAAA --

```

Fig. 4 UL131-128 mRNA processing – Panels (A-C) compare FIX-BAC DNA sequence (numbered according to Chee et al.) to a set of cDNA sequences from RACE clones 95-3, 95-8 and 95-11 (A) UL131 region, (B) UL128 region, (C) UL131-128 transcripts 3' end. Start codons, stop codons and the polyA site are in bold face, mRNA processing signals (splice donor sequence, splice acceptor sequence, AATAAA signal) are grey-shaded.





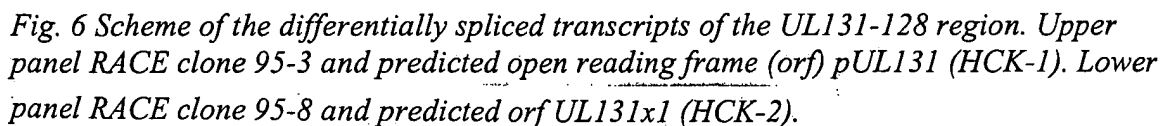
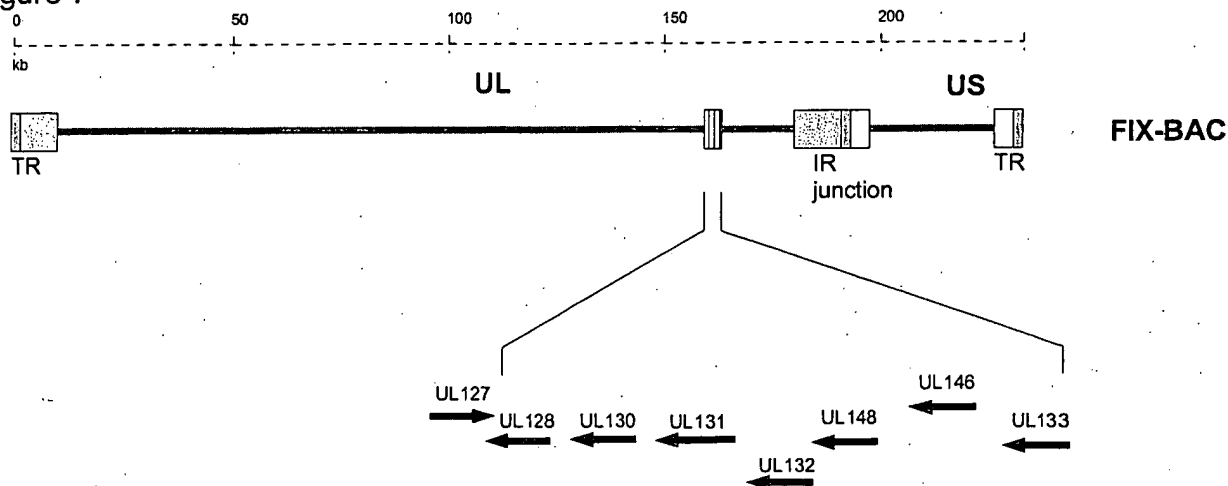


Figure 7

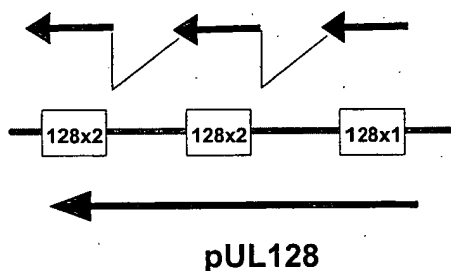


#### Translation of SEQ128.txt(1-563 : HCK-4 (pUL128)

```

1      ATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTATHEGTCACAGC
1      M S P K N L T P F L T A L W L L L G H S
61     CGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCAACCACCCGCCG
21     R V P R V R A E E C C E F I N V N H P P
121    GAACGCTGTACGATTTCAAAATGTGCAATCGCTTCACCGTCGCACGTGCGGTGTCCGGAC
41     E R C Y D F K M C N R P T V A L R C P D
181    GCGAAGTCTGCTACAGTCCCGAGAAACGGCTGAGATTTCGCGGGATCGTCACCACCATG
61     G E V C Y S P E K T A E I R G I V T T M
241    ACCCATTCATTGACACGCCAGGTCTGTACACAACAACTGACGAGCTGCAACTACAATCTG
81     T H S L T R Q V V H N K L T S C N Y N L
301    TTATACCTCGAAGCTGACGGGCGAATACGCTCGCGCAAAGTGAACGACAAGGCGCAGTAC
101    L Y L E A D G R I R C G K V N D K A Q Y
361    CTGCTGGGCGCGCTGGCAGCGTTCCCTATCGATGGATCAACCTGGAATACGACAAGATA
121    L L G A A G S V P Y R W I N L E Y D K I
421    ACCCGGATCGTGGGCTGGATCAGTACCTGGAGAGCGTTAAGAAACACAAACGGCTGGAT
141    T R I V G L D Q Y L E S V K K H K R L D
481    GTGTCCCGCGCTAAAATGGGCTATATGCTGCAGTGA
161    V C R A K M G Y M L Q *

```



#### Translation of SEQ128 x 1.txt HCK-3 (pUL128x1)

```

1      ATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTATTGGGTCACAGC
1      M S P K N L T P F L T A L W L L L G H S
61     CGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCAACCACCCGCCG
21     R V P R V R A E E C C E F I N V N H P P
121    GAACGCTGTACGATTTCAAAATGTGCAATCGCTTCACCGTCGCGTACGTATTTTCATGA
41     E R C Y D F K M C N R P T V A Y V F S *

```

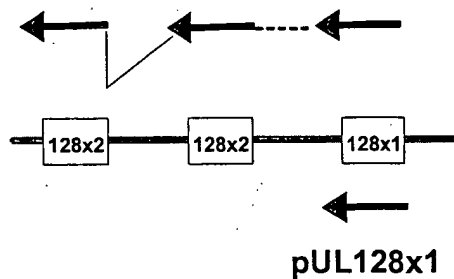


Fig. 7 Scheme of the differentially spliced transcripts of the UL131-128 region. Upper panel SEQUL128B and predicted open reading frame (orf) pUL128 (HCK-4). Lower panel SEQUL128A and predicted orf UL128x1 (HCK-3).

Figure 8

### Northern Blot Analyses

RVFIX, RVFIX mutants and laboratory strains:

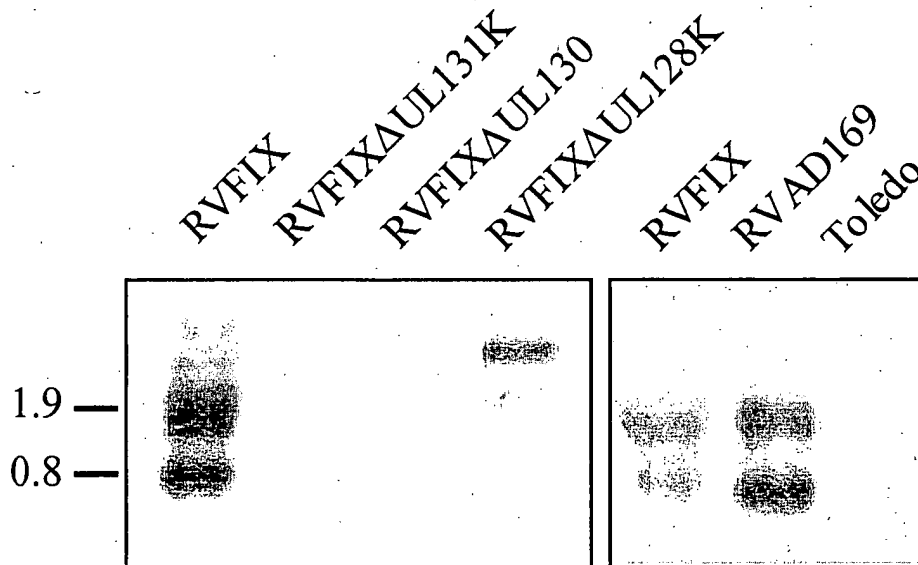


Fig. 8 mRNA was prepared from RVFIX-infected fibroblasts 4 days p.i. using Rneasy Mini, QIAshredder and Oligotex mRNA Mini kits according to the manufacturer's guidance (Qiagen). For Northern blotting, 1  $\mu$ g RNA was electrophoresed on an agarose gel according to the MOPS-formaldehyde protocol and blotted onto Hybond N+ membranes (Amersham Pharmacia). Blots were hybridized with a UL131-128 specific probe.

Figure 9

## Comparison RACE clone 95-3 – FIX genomic sequence

Upper line: SEQFIX UL131-128.txt, from 10 to 1977

Lower line: SEQKlon95-3.txt, from 1 to 1741

SEQFIX UL131-128.txt:SEQKlon95-3.txt identity= 99.66%(1735/1741)  
 gap=11.94%(236/1977)

```

1      GTCTGCAACATGCGGCTGTGTCGGGTGTGGCTGTCTGTTTGTCTGTGCGCCGTGGTGCTG
      |||
1      .....ATGCGGCTGTCTCGGGTGTGGCTGTCTGTTTGTCTGTGCGCCGTGGTGCTG

61     GGTCAAGTGCAGCGGGAGACCGCAGAAAAAACGATTATTACCGAGTACCGCATTACTGG
      |||
52     GGTCAAGTGCAGCGGGAGACCGCAGAAAAAACGATTATTACCGAGTACCGCATTACTGG

121    GACGCGTGCTCTCGCGCGCTGCCTGACCAAACCCGTTACAAGTATGTGGAACAGCTCGTG
      |||
112    GACGCGTGCTCTCGCGCGCTGCCTGACCAAACCCGTTACAAGTATGTGGAACAGCTCGTG

181    GACCTCACGTTGAACTACCACTACGATGCGAGCCACGGCTTGGACAACCTTTGACGTGCTC
      |||
172    GACCTCACGTTGAACTACCACTACGATGCGAGCCACGGCTTGGACAACCTTTGACGTGCTC

241    AAGAGGTGAGGGTACGCGCTAAAGGTGTATGACAACGGGAAGGTAAGGGCGAACGGGTAA
      |||
232    AAGAG.....

301    CGGGTAGGTAACCGCATGGGGTGTGAAATGACGTTTCGGAACCTGTGCTTGCAGAATCAAC
      |||
235    .....AATCAAC

361    GTGACCGAGGTGTCGTTGCTCATCAGCGACTTTAGACGTCAGAACCGTCGCGGCGGCACC
      |||
244    GTGACCGAGGTGTCGTTGCTCATCAGCGACTTTATACGTCAGAACCGTCGCGGCGGCACC

421    AACAAAAGGACCACGTTCAACGCCGCCGGTTCGCTGGCGCCTCACGCCCCGAGCCTCGAG
      |||
304    AACAAAAGGACCACGTTCAACGCCGCCGGTTCGCTGGCGCCTCACGCCCCGAGCCTCGAG

481    TTCAGCGTGCGGCTCTTTGCCAACTAGCCTGCGTCACGGGAAATAATATGCTACGGCTTC
      |||
364    TTCAGCGTGCGGCTCTTTGCCAACTAGCCTGCGTCACGGGAAATAATATGCTACGGCTTC

541    TGCTTCGTCACCACTTTCAGTGCCTGCTTCTGTGCGCGGTTTGGGCAACGCCCTGTCTGG
      |||
424    TGCTTCGTCACCACTTTCAGTGCCTGCTTCTGTGCGCGGTTTGGGCAACGCCCTGTCTGG

601    CGTCTCCGTGGTTTCACGCTAACGGCGAACCAGAAATCCGTCCCCGCCATGGTCTAAACTGA
      |||

```

484 CGTCTCCGTGGTTACGCTAACGGCGAACCAGAATCCGTCCCCGCCATGGTCTAAACTGA  
 661 CGTATCCCAAACCGCATGACGCGGCGACGTTTTACTGTCTTTTCTCTATCCCTCGCCCC  
 |||||  
 544 CGTATCCCAAACCGCATGACGCGGCGACGTTTTACTGTCTTTTCTCTATCCCTCGCCCC  
 721 CACGGTCCCCCTCGCAATTCCCGGGGTCCAGCGGGTATCAACGGGTCCCGAGTGTGCGCA  
 |||||  
 604 CACGGTCCCCCTCGCAATTCCCGGGGTCCAGCGGGTATCAACGGGTCCCGAGTGTGCGCA  
 781 ACGAGACCCTGTATCTGCTGTACAACCGGGAAGGCCAGACCTTGGTGGAGAGAAGCTCCA  
 |||||  
 664 ACGAGACCCTGTATCTGCTGTACAACCGGGAAGGCCAGACCTTGGTGGAGAGAAGCTCCA  
 841 CCTGGGTGAAAAAGGTGATCTGGTATCTGAGCGGTCGCAATCAGACCATCCTCCAACGGA  
 |||||  
 724 CCTGGGTGAAAAAGGTGATCTGGTATCTGAGCGGTCGCAATCAGACCATCCTCCAACGGA  
 901 TGCCCCGAACGGCTTCGAAACCGAGCGACGGAAACGTGCAGATCAGCGTGAAGACGCCA  
 |||||  
 784 TGCCCCGAACGGCTTCGAAACCGAGCGACGGAAACGTGCAGATCAGCGTGAAGACGCCA  
 961 AGATTTTTGGAGCGCACATGGTGCCCAAGCAGACCAAGCTGCTACGTTTCGTCGTCACCG  
 |||||  
 844 AGATTTTTGGAGCGCACATGGTGCCCAAGCAGACCAAGCTGCTACGTTTCGTCGTCACCG  
 1021 ATGGCACACGTTATCAGATGTGTGTGATGAAACTGGAGAGCTGGGCCCACGTCTTCCGGG  
 |||||  
 904 ATGGCACACGTTATCAGATGTGTGTGATGAAACTGGAGAGCTGGGCCCACGTCTTCCGGG  
 1081 ACTACAGCGTGTCTTTTCAGGTGCGATTGACGTTACCGAGGCCAATAACCAGACTTACA  
 |||||  
 964 ACTACAGCGTGTCTTTTCAGGTGCGATTGACGTTACCGAGGCCAATAACCAGACTTACA  
 1141 CCTTCTGCACCCATCCCAATCTCATCGTTTGAGCCCGTCGCGCGCGCAGGGAATTTTGAA  
 |||||  
 1024 CCTTCTGCACCCATCCCAATCTCATCGTTTGAGCCCGTCGCGCGCGCAGGGAATTTTGAA  
 1201 AACCGCGCGTCATGAGTCCCCAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTAT  
 |||||  
 1084 AACCGTGCCTCATGAGTCCCCAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTAT  
 1261 TGGGTACAGCCGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCA  
 |||||  
 1144 TGGGTACAGCCGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCA  
 1321 ACCACCCGCCGGAACGCTGTTACGATTTCAAATGTGCAATCGCTTCACCGTCGCGTACG  
 |||||  
 1204 ACCACCCGCCGGAACGCTGTTACGATTTCAAATGTGCAATCGCTTCACCGTCGCGTACG  
 1381 TATTTTCATGATTGTCTGCGTTCTGTGGTGCGTCTGGATTTGTCTCTCGACGTTTCTGAT  
 |||||  
 1264 TATTTTCATGATTGTCTGCGTTCTGTGGTGCGTCTGGATCTGTCTCTCGACGTTTCTGAT  
 1441 AGCCATGTTCCATCGACGATCCTCGGGAATGCCAGAGTAGATTTTCATGAATCCACAGGC  
 |||||  
 1324 AGCCATGTTCCATCGACGATCCTCGGGAATGCCAGAGTAGATTTTCATGAATCCACAGGC

1501 TCGGGTGTCCGGACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTTCGCGGGA  
 |||||  
 1384 TCGGGTGTCCGGACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTTCGCGGGA  
 |||||  
 1561 TCGTCACCACCATGACCCATTTCATTGACACGCCAGGTCGTACACAACAACTGACGAGCT  
 |||||  
 1444 TCGTCACCACCATGACCCATTTCATTGACACGCCAGGTCGTACACAACAACTGACGAACT  
 |||||  
 1621 GCAACTACAATCCGTAAGTCTCTTCCTCGAGGGCCTTACAGCCTATGGGAAAAGTAAGACA  
 |||||  
 1504 GCAACTACAATCC.....  
 1681 GAGGGACAAAACATCATTAAAAAAAAGTCTAATTTACGTTTTGTACCCCCCTTCCCC  
 1517 .....  
 1741 TCCGTGTTGTAGGTTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAACGA  
 |||||  
 1517 .....GTTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAACGA  
 1801 CAAGGCGCAGTACCTGCTGGGCGCCGCTGGCAGCGTTCCCTATCGATGGATCAACCTGGA  
 |||||  
 1565 CAAGGCGCAGTACCTGCTGGGCGCCGCTGGCAGCGTTCCCTATCGATGGATCAACCTGGA  
 1861 ATACGACAAGATAACCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAACA  
 |||||  
 1625 ATACGACAAGATAACCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAACA  
 1921 CAAACGGCTGGATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAA  
 |||||  
 1685 CAAACGGCTGGATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAA

### Translation of SEQKlon95-3.txt: HCK-1 (pUL131)

1 ATGCGGCTGTCTCGGGTGTGGCTGTCTGTTTGTCTGTGCGCCGTGGTGCTGGGTCAAGTGC  
 1 M R L S R V W L S V C L C A V V L G Q C  
 61 CAGCGGGAGACCGCAGAAAAAACGATTATTACCGAGTACCGCATTACTGGGACGCGTGC  
 21 Q R E T A E K N D Y Y R V P H Y W D A C  
 121 TCTCGCGCGCTGCCTGACCAAACCCGTTACAAGTATGTGGAACAGCTCGTGGACCTCACG  
 41 S R A L P D Q T R Y K Y V E Q L V D L T  
 181 TTGAACTACCACTACGATGCGAGCCACGGCTTGGAACAACCTTTGACGTGCTCAAGAGAATC  
 61 L N Y H Y D A S H G L D N F D V L K R I  
 241 AACGTGACCGAGGTGTCTGTTGCTCATCAGCGACTTTTATACGTCAGAACCGTCGCGGCGGC  
 81 N V T E V S L L I S D F I R Q N R R G G  
 301 ACCAACAAAAGGACCACGTTCAACGCCGCCGGTTCGCTGGCGCCTCACGCCCCGAGCCTC  
 101 T N K R T T F N A A G S L A P H A R S L  
 361 GAGTTCAGCGTGCGGCTCTTTGCCAACTAG  
 121 E F S V R L F A N \*

**Figure 10****Comparison RACE clone 95-8 –FIX genomic sequence****Upper line: SEQFIX UL131-128.txt, from 10 to 1977****Lower line: SEQKlon95-8.txt, from 1 to 1849**

SEQFIX UL131-128.txt:SEQKlon95-8.txt identity= 99.78%(1845/1849)  
 gap=6.47%(128/1977)

```

1   GTCTGCAACATGCGGCTGTGTCGGGTGTGGCTGTCTGTTTGTCTGTGCGCCGTGGTGCTG
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1   .....ATGCGGCTGTGTCGGGTGTGGCTGTCTGTTTGTCTGTGCGCCGTGGTGCTG

61  GGTTCAGTGCCAGCGGGAGACCGCAGAAAAAACGATTATTACCGAGTACCGCATTACTGG
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
52  GGTTCAGTGCCAGCGGGAGACCGCAGAAAAAACGATTATTACCGAGTACCGCATTACTGG

121 GACGCGTGCTCTCGCGCGCTGCCTGACCAAACCCGTTACAAGTATGTGGAACAGCTCGTG
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
112 GACGCGTGCTCTCGCGCGCTGCCTGACCAAACCCGTTACAAGTATGTGGAACAGCTCGTG

181 GACCTCACGTTGAACTACCACTACGATGCGAGCCACGGCTTGGACAACCTTTGACGTGCTC
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
172 GACCTCACGTTGAACTACCACTACGATGCGAGCCACGGCTTGGACAACCTTTGACGTGCTC

241 AAGAGGTGAGGGTACGCGCTAAAGGTGTATGACAACGGGAAGGTAAGGGCGAACGGGTAA
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
232 AAGAGGTGAGGGTACGCGCTAAAGGTGTATGACAACGGGAAGGTAAGGGCGAACGGGTAA

301 CGGGTAGGTAACCGCATGGGGTGTGAAATGACGTTTCGGAACCTGTGCTTGCAGAATCAAC
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
292 CGGGTAGGTAACCGCATGGGGTGTGAAATGACGTTTCGGAACCTGTGCTTGCAGAATCAAC

361 GTGACCGAGGTGTCGTTGCTCATCAGCGACTTTAGACGTCAGAACCGTCGCGGCGGCACC
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
352 GTGACCGAGGTGTCGTTGCTCATCAGCGACTTTAGACGTCAGAACCGTCGCGGCGGCACC

421 AACAAAAGGACCACGTTCAACGCCGCCGGTTTCGCTGGCGCCTCACGCCCCGAGCCTCGAG
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
412 AACAAAAGGACCACGTTCAACGCCGCCGGTTTCGCTGGCGCCTCACGCCCCGAGCCTCGAG

481 TTCAGCGTGCGGCTCTTTTGCCAACTAGCCTGCGTCACGGGAAATAATATGCTACGGCTTC
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
472 TTCAGCGTGCGGCTCTTTTGCCAACTAGCCTGCGTCACGGGAAATAATATGCTACGGCTTC

541 TGCTTCGTCACCACTTTCACTGCCTGCTTCTGTGCGCGGTTTGGGCAACGCCCTGTCTGG
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
532 TGCTTCGTCACCACTTTCACTGCCTGCTTCTGTGCGCGGTTTGGGCAACGCCCTGTCTGG

```

601 CGTCTCCGTGGTTCACGCTAACGGCGAACCAGAAATCCGTCCCCGCCATGGTCTAAACTGA  
 |||||  
 592 CGTCTCCGTGGTTCACGCTAACGGCGAACCAGAAATCCGTCCCCGCCATGGTCTAAACTGA  
 |||||  
 661 CGTATCCCAAACCGCATGACGCGGCGACGTTTTACTGTCTTTTCTCTATCCCTCGCCCC  
 |||||  
 652 CGTATCCCAAACCGCATGACGCGGCGACGTTTTACTGTCTTTTCTCTATCCCTCGCCCC  
 |||||  
 721 CACGGTCCCCCTCGCAATTCCCGGGGTTCAGCGGGTATCAACGGGTCCCGAGTGTGCGCA  
 |||||  
 712 CACGGTCCCCCTCGCAATTCCCGGGGTTCAGCGGGTATCAACGGGTCCCGAGTGTGCGCA  
 |||||  
 781 ACGAGACCCTGTATCTGCTGTACAACCGGGAAGGCCAGACCTTGGTGGAGAGAAGCTCCA  
 |||||  
 772 ACGAGACCCTGTATCTGCTGTACAACCGGGAAGGCCAGACCTTGGTGGAGAGAAGCTCCA  
 |||||  
 841 CCTGGGTGAAAAAGGTGATCTGGTATCTGAGCGGTCGCAATCAGACCATCCTCCAACGGA  
 |||||  
 832 CCTGGGTGAAAAAGGTGATCTGGTATCTGAGCGGTCGCAATCAGACCATCCTCCAACGGA  
 |||||  
 901 TGCCCCGAACGGCTTCGAAACCGAGCGACGGAACGTGCAGATCAGCGTGAAGACGCCA  
 |||||  
 892 TGCCCCGAACGGCTTCGAAACCGAGCGACGGAACGTGCAGATCAGCGTGAAGACGCCA  
 |||||  
 961 AGATTTTTGGAGCGCACATGGTGCCCAAGCAGACCAAGCTGCTACGTTTCGTCGTC AACG  
 |||||  
 952 AGATTTTTGGAGCGCACATGGTGCCCAAGCAGACCAAGCTGCTACGTTTCGTCGTC AACG  
 |||||  
 1021 ATGGCACACGTTATCAGATGTGTGTGATGAACTGGAGAGCTGGGCCCACGTCTTCCGGG  
 |||||  
 1012 ATGGCACACGTTATCAGATGTGTGTGATGAACTGGAGAGCTGGGCCCACGTCTTCCGGG  
 |||||  
 1081 ACTACAGCGTGTCTTTTCAGGTGCGATTGACGTTACCGAGGCCAATAACCAGACTTACA  
 |||||  
 1072 ACTACAGCGTGTCTTTTCAGGTGCGATTGACGTTACCGAGGCCGATAACCAGACTTACA  
 |||||  
 1141 CCTTCTGCACCCATCCCAATCTCATCGTTTGAGCCCGTCGCGCGCGCAGGGAATTTTGAA  
 |||||  
 1132 CCTTCTGCACCCATCCCAATCTCATCGTTTGAGCCCGTCGCGCGCGCAGGGAATTTTGAA  
 |||||  
 1201 AACC GCGCGTCATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTAT  
 |||||  
 1192 AACC GCGCGTCATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTAT  
 |||||  
 1261 TGGGTCACAGCCGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCA  
 |||||  
 1252 TGGGTCACAGCCGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCA  
 |||||  
 1321 ACCACCCGCCGGAACGCTGTTACGATTTCAAAATGTGCAATCGCTTCACCGTCGCGTACG  
 |||||  
 1312 ACCACCCGCCGGAACGCTGTTACGATTTCAAAATGTGCAATCGCTTCACCGTCGCGTACG  
 |||||  
 1381 TATTTTCATGATTGTCTGCGTTCTGTGGTGCGTCTGGATTTGTCTCTCGACGTTTCTGAT  
 |||||  
 1372 TATTTTCATGATTGTCTGCGTTCTGTGGTGCGTCTGGATCTGTCTCTCGACGTTTCTGAT  
 |||||



```

1441 AGCCATGTTCCATCGACGATCCTCGGGAATGCCAGAGTAGATTTTCATGAATCCACAGGC
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1432 AGCCATGTTCCATCGACGATCCTCGGGAATGCCAGAGTAGATTTTCATGAATCCACAGGC

1501 TCGCGGTGTCCGGACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTTCGCGGGA
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1492 TCGCGGTGTCCGGACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTTCGCGGGA

1561 TCGTCACCACCATGACCCATTTCATTGACACGCCAGGTTCGTACACAACAACTGACGAGCT
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1552 TCGTCACCACCATGACCCATTTCATTGACACGCCAGGTTCGTACACAACAACTGACGAGCT

1621 GCAACTACAATCCGTAAGTCTCTTCTCGAGGGCCTTACAGCCTATGGGAAAGTAAGACA
      ||||||||||||
1612 GCAACTACAATCC.....

1681 GAGGGACAAAACATCATTAAAAAAAAGTCTAATTTACGTTTTGTACCCCCCTTCCCC
1625 .....

1741 TCCGTGTTGTAGGTTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAACGA
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1625 .....GTTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAACGA

1801 CAAGGCGCAGTACCTGCTGGGCGCCGCTGGCAGCGTTCCTATCGATGGATCAACCTGGA
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1673 CAAGGCGCAGTACCTGCTGGGCGCCGCTGGCAGCGTTCCTATCGATGGATCAACCTGGA

1861 ATACGACAAGATAACCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAACA
      |||||||||||| ||||||||||||||||||||||||||||||||||||||||
1733 ATACGACAAGATAGCCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAACA

1921 CAAACGGCTGGATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAA
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1793 CAAACGGCTGGATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAA

```

### Translation of SEQKlon95-8.txt: HCK-2 (pUL131x1)

```

1      ATGCGGCTGTGTGCGGTGTGGCTGTCTGTTTGTCTGTGCGCCGTGGTGCTGGGTCAAGTGC
1      M R L C R V W L S V C L C A V V L G Q C

61      CAGCGGGAGACCGCAGAAAAAACCATTATTACCGAGTACCGCATTACTGGGACGCGTGC
21      Q R E T A E K N D Y Y R V P H Y W D A C

121     TCTCGCGCGCTGCCTGACCAAACCCGTTACAAGTATGTGGAACAGCTCGTGGACCTCAGG
41      S R A L P D Q T R Y K Y V E Q L V D L T

181     TTGAACTACCACTACGATGCGAGCCACGGCTTGGACAACCTTTGACGTGCTCAAGAGGTGA
61      L N Y H Y D A S H G L D N F D V L K R *

```

**Figure 11****Comparison RACE clone 95-11 –FIX genomic sequence****Upper line: SEQFIX UL131-128.txt, from 10 to 1977****Lower line: SEQKlon95-11.txt, from 1 to 1620**

SEQFIX UL131-128.txt:SEQKlon95-11.txt identity= 99.57%(1611/1618)  
 gap=18.24%(361/1979)

```

1      GTCTGCAACATGCGGCTGTGTCTGGGTGTGGCTGTCTGTTTGTCTGTGCGCCGTGGTGCTG
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1      .....ATGCGGCTGTGTCTGGGTGTGGCTGTCTGTTTGTCTGTGCGCCGTGGTGCTG

61     GGTCAAGTGCCAGCGGGAGACCGCAG...AAAAAACGATTATTACCGAGTACCGCATTACT
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
52     GGTCAAGTGCCAGCGGGAGACCGCAGAAAAAAAACGATTATTACCGAGTACCGCATTACT

119    GGGACGCGTGCTCTCGCGCGCTGCCTGACCAAACCCGTTACAAGTATGTGGAACAGCTCG
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
112    GGGACGCGTGCTCTCGCGCGCTGCCTGACCAAACCCGTTACAAGTATGTGGAACAGCTCG

179    TGGACCTCACGTTGAACTACCACTACGATGCGAGCCACGGCTTGGACAACCTTTGACGTGC
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
172    TGGACCTCACGTTGAACTACCACTACGATGCGAGCCACGGCTTGGACAACCTTTGACGTGC

239    TCAAGAGGTGAGGGTACGCGCTAAAGGTGTATGACAACGGGAAGGTAAGGGCGAACGGGT
      |||||||
232    TCAAGAG.....

299    AACGGGTAGGTAACCGCATGGGGTGTGAAATGACGTTTCGGAACCTGTGCTTGCAGAATCA
      ||||||
237    .....AATCA

359    ACGTGACCGAGGTGTCTGTTGCTCATCAGCGACTTTAGACGTCAGAACCGTCGCGGCGGCA
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
244    ACGTGACCGAGGTGTCTGTTGCTCATCAGCGACTTTAGACGTCAGAACCGTCGCGGCGGCA

419    CCAACAAAAGGACCACGTTCAACGCCGCCGGTTTCGCTGGCGCCTCACGCCCCGAGCCTCG
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
304    CCAACAAAAGGACCACGTTCAACGCCGCCGGTTTCGCTGGCGCCTCACGCCCCGAGCCTCG

479    AGTTCAGCGTGCGGCTCTTTTGCCAACTAGCCTGCGTCACGGGAAATAATATGCTACGGCT
      |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
364    AGTTCAGCGTGCGGCTCTTTTGCCAACTAGCCTGCGTCACGGGAAATAATATGCTACGGCT

539    TCTGCTTCGTACCACTTTCACTGCCTGCTTCTGTGCGCGGTTTGGGCAACGCCCTGTCT

```

424 |||||TCTGCTTCGTCACCACTTTCACTGCCTGCTTCTGTGCGCGGTTTGGGCAACGCCCTGTCT  
 599 GCGTCTCCGTGGTTACGCTAACGGCGAACCAGAATCCGTCCCCGCCATGGTCTAAACT  
 484 |||||GCGTCTCCGTGGTTACGCTAACGGCGAACCAGAATCCGTCCCCGCCATGGTCTAAACT  
 659 GACGTATCCCAAACCGCATGACGCGGCGACGTTTTACTGTCCTTTTCTCTATCCCTCGCC  
 544 |||||GACGTATCCCAAACCGCATGACGCGGCGACGTTTTACTGTCCTTTTCTCTATCCCTCGCC  
 719 CCCACGGTCCCCCTCGCAATTCCCGGGGTTCAGCGGGTATCAACGGGTCCCGAGTGTCTG  
 604 |||||CCCACGGTCCCCCTCGCAATTCCCGGGGTTCAGCGGGTATTAACGGGTCCCGAGTGTCTG  
 779 CAACGAGACCCTGTATCTGCTGTACAACCGGGAAGGCCAGACCTTGGTGGAGAGAAGCTC  
 664 |||||CAACGAGACCCTGTATCTGCTGTACAACCGGGAAGGCCAGACCTTGGTGGAGAGAAGCTC  
 839 CACCTGGGTGAAAAAGGTGATCTGGTATCTGAGCGGTGCAATCAGACCATCCTCCAACG  
 724 |||||CACCTGGGTGAAAAAGGTGATCTGGTATCTGAGCGGTGCAATCAGACCATCCTCCAACG  
 899 GATGCCCCGAACGGCTTCGAAACCGAGCGACGGAAACGTGCAGATCAGCGTGAAGACGC  
 784 |||||GATGCCCCGAACGGCTTCGAAACCGAGCGACGGAAACGTGCAGATCAGCGTGAAGACGC  
 959 CAAGATTTTTGGAGCGCACATGGTGCCCAAGCAGACCAAGCTGCTACGTTTCGTCTGCAA  
 844 |||||CAAGATTTTTGGAGCGCACATGGTGCCCAAGCAGACCAAGCTGCTACGTTTCGTCTGCAA  
 1019 CGATGGCACACGTTATCAGATGTGTGTGATGAAACTGGAGAGCTGGGCCCACGTCTTCCG  
 904 |||||CGATGGCACACGTTATTAGATGTGTGTGATGAAACTGGAGAGCTGGGCCCACGTCTTCCG  
 1079 GGACTACAGCGTGTCTTTTCAGGTGCGATTGACGTTACCGAGGCCAATAACCAGACTTA  
 964 |||||GGACTACAGCGTGTCTTTTCAGGTGCGATTGACGTTACCGAGGCCAATAACCAGACTTA  
 1139 CACCTTCTGCACCCATCCCAATCTCATCGTTTGAGCCCGTCGCGCGCAGGGAATTTTG  
 1024 |||||CACCTTCTGCACCCATCCCAATCTCATCGTTTGAGCCCGTCGCGCGCAGGGAATTTTG  
 1199 AAAACCGCGCGTCATGAGTCCCCAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCT  
 1084 |||||AAAACCGCGCGTCATGAGTCCCCAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCT  
 1259 ATTGGGTACAGCCGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGT  
 1144 |||||ATTGGGTACAGCCGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGT  
 1319 CAACCACCCGCCGGAACGCTGTTACGATTTCAAAATGTGCAATCGCTTCACCGTCGCGTA  
 1204 |||||CAACCACCCGCCGGAACGCTGTTACGATTTCAAAATGTGCAATCGCTTCACCGTCGC..  
 1379 CGTATTTTCATGATTGTCTGCGTTCTGTGGTGCGTCTGGATTTGTCTCTCGACGTTTCTG

1262 .....  
 1439 ATAGCCATGTTCCATCGACGATCCTCGGGAATGCCAGAGTAGATTTTCATGAATCCACAG  
 1262 .....  
 1499 GCTGCGGTGTCCGGACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTGCGCGG  
 |||||  
 1262 ACTGCGGTGTCCGGACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTGCGCGG  
 1559 GATCGTCACCACCATGACCCATTCATTGACACGCCAGGTCGTACACAACAACTGACGAG  
 |||||  
 1321 GATCGTCACCACCATGACCCATTCATTGACACGCCAGGTCGTACACAACAACTGACGAG  
 1619 CTGCAACTACAATCCGTAAGTCTCTTCTCGAGGGCCTTACAGCCTATGGGAAAGTAAGA  
 |||||  
 1381 CTGCAACTACAATCT.....  
 1679 CAGAGGGACAAAACATCATTAATAAAAAAAGTCTAATTTACGTTTTGTACCCCCCTTCC  
 1396 .....  
 1739 CCTCCGTGTTGTAGGTTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAAC  
 |||||  
 1396 .....GTTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAAC  
 1799 GACAAGGCGCAGTACCTGCTGGGCGCCGCTGGCAGCGTTCCTATCGATGGATCAACCTG  
 |||||  
 1442 GACAAGGCGCAGTACCTGCTGGGCGCCGCTGGCAGCGTTCCTATCGATGGATCAACCTG  
 1859 GAATACGACAAGATAACCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAA  
 |||||  
 1502 GAATACGACAAGATAACCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAA  
 1919 CACAAACGGCTGGATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAA  
 |||||  
 1562 TACAAACGGCTGGATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAA

*Figure 12***Comparison SEQ 128 B - FIX genomic sequence**

Upper line: FIX genomic sequence

Lower line: SEQ 128 B

```

5998  ATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTATTGGGTCACAGC
      |||
1      ATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTATTGGGTCACAGC

6058  CGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCAACCACCCGCCG
      |||
61     CGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCAACCACCCGCCG

6118  GAACGCTGTTACGATTTCAAAATGTGCAATCGCTTCACCGTCGCGTACGTATTTTCATGA
      |||
121    GAACGCTGTTACGATTTCAAAATGTGCAATCGCTTCACCGTCGCGTACGTATTTTCATGA

6178  TTGTCTGCGTTCTGTGGTGCGTCTGGATCTGTCTCTCGACGTTTCTGATAGCCATGTTCC
      |||
181    TTGTCTGCGTTCTGTGGTGCGTCTGGATCTGTCTCTCGACGTTTCTGATAGCCATGTTCC

6238  ATCGACGATCCTCGGGAATGCCAGAGTAGATTTTCATGAATCCACAGGCTGCGGTGTCCG
      |||
241    ATCGACGATCCTCGGGAATGCCAGAGTAGATTTTCATGAATCCACAGGCTGCGGTGTCCG

6298  GACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTGCGGGGATCGTCACCACC
      |||
301    GACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTGCGGGGATCGTCACCACC

6358  ATGACCCATTCAATTGACACGCCAGGTCGTACACAACAACTGACGAGCTGCAACTACAAT
      |||
361    ATGACCCATTCAATTGACACGCCAGGTCGTACACAACAACTGACGAGCTGCAACTACAAT

6418  CCGTAAGTCTCTTCCTCGAGGGCCTTACAGCCTATGGGAAAGTAAGACAGAGGGACAAAA
      ||
421    CC.....

6478  CATCATTAATAAAAAAAGTCTAATTTACGTTTTGTACCCCCCTTCCCCTCCGTGTTGTA
      ||
423    .....

```

```

6538 GGT TATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAACGACAAGGCGCAGT
      |||
423  .GTTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAACGACAAGGCGCAGT

6598 ACCTGCTGGGCGCCGCTGGCGGCGTTCCCTATCGATGGATCAACCTGGAATACGACAAGA
      |||
482  ACCTGCTGGGCGCCGCTGGCGGCGTTCCCTATCGATGGATCAACCTGGAATACGACAAGA

6658 TAGCCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAACACAAACGGCTGG
      |||
542  TAGCCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAACACAAACGGCTGG

6718 ATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAAATGTGTGTTTGTCC
      |||
602  ATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAAATGTGTGTTTGTCC

6778 GAAATACGCGTTTTTGAGATTTCTG
      |||
662  AAAAAAAAAAAAAAAAAAAAAA

```

**Translation of SEQ128 B x 1.txt: HCK-3 (pUL128x1)**

```

1      ATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTATTGGGTCACAGC
1      M S P K N L T P F L T A L W L L L G H S

61     CGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCAACCACCCGCCG
21     R V P R V R A E E C C E F I N V N H P P

121    GAACGCTGTTACGATTTCAAAATGTGCAATCGCTTCACCGTCGCGTACGTATTTTCATGA
41     E R C Y D F K M C N R F T V A Y V F S *

```

Figure 13

**Comparison SEQ 128 A - FIX genomic sequence****Upper line: FIX-BAC****Lower line: SEQ128 A**

```

5998  ATGAGTCCCAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTATTGGGTCACAGC
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1      ATGAGTCCCAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTATTGGGTCACAGC

6058  CGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCAACCACCCGCCG
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
61      CGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCAACCACCCGCCG

6118  GAACGCTGTTACGATTTCAAAATGTGCAATCGCTTCACCGTCGCGTACGTATTTTATGA
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
121    GAACGCTGTTACGATTTCAAAATGTGCAATCGCTTCACCGTCGC.....

6178  TTGTCTGCGTTCTGTGGTGCGTCTGGATTTGTCTCTCGACGTTTCTGATAGCCATGTTCC

166    .....

6238  ATCGACGATCCTCGGGAATGCCAGAGTAGATTTTCATGAATCCACAGGCTGCGGTGTCCG
      |||||||||||||||
166    .....GCTGCGGTGTCCG

6298  GACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTGCGCGGGATCGTCACCACC
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
178    GACGGCGAAGTCTGCTACAGTCCCGAGAAAACGGCTGAGATTGCGCGGGATCGTCACCACC

6358  ATGACCCATTCAATTGACACGCCAGGTCGTACACAACAACTGACGAGCTGCAACTACAAT
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
238    ATGACCCATTCAATTGACACGCCAGGTCGTACACAACAACTGACGAGCTGCAACTACAAT

6418  CCGTAAGTCTCTTCCTCGAGGGCCTTACAGCCTATGGGAAAGTAAGACAGAGGGACAAAA
      ||
298    CC.....

6478  CATCATTAATAAAAAAGTCTAATTTACGTTTTGTACCCCCCTTCCCCTCCGTGTTGTA

300    .....

6538  GGTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAACGACAAGGCGCAGT
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
300    .GTTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAACGACAAGGCGCAGT

6598  ACCTGCTGGGCGCCGCTGGCAGCGTTCCCTATCGATGGATCAACCTGGAATACGACAAGA
      ||||||||||||||||||||||||||||||||||||||||||||||||||||

```

359 ACCTGCTGGGCGCCGCTGGCAGCGTTCCCTATCGATGGATCAACCTGGAATACGACAAGA  
 6658 TAACCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAACACAAACGGCTGG  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 419 TAACCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAACACAAACGGCTGG  
 6718 ATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAAATGTGTGTTTGTCC  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 479 ATGTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGAATAATAAAATGTG

**Translation of SEQ128 A: HCK-4 (pUL128)**

1 ATGAGTCCCAAAAACCTGACGCCGTTCTTGACGGCGTTGTGGCTGCTATTGGGTCACAGC  
 1 M S P K N L T P F L T A L W L L L G H S  
 61 CGCGTGCCGCGGGTACGCGCAGAAGAATGTTGCGAATTCATAAACGTCAACCACCCGCCG  
 21 R V P R V R A E E C C E F I N V N H P P  
 121 GAACGCTGTTACGATTTCAAATGTGCAATCGCTTCACCGTCGCACTGCGGTGTCCGGAC  
 41 E R C Y D F K M C N R F T V A L R C P D  
 181 GGCGAAGTCTGCTACAGTCCCGAGAAACGGCTGAGATTCGCGGGATCGTCACCACCATG  
 61 G E V C Y S P E K T A E I R G I V T T M  
 241 ACCCATTCATTGACACGCCAGGTCGTACACAACAACTGACGAGCTGCAACTACAATCTG  
 81 T H S L T R Q V V H N K L T S C N Y N L  
 301 TTATACCTCGAAGCTGACGGGCGAATACGCTGCGGCAAAGTGAACGACAAGGCGCAGTAC  
 101 L Y L E A D G R I R C G K V N D K A Q Y  
 361 CTGCTGGGCGCCGCTGGCAGCGTTCCCTATCGATGGATCAACCTGGAATACGACAAGATA  
 121 L L G A A G S V P Y R W I N L E Y D K I  
 421 ACCCGGATCGTGGGCCTGGATCAGTACCTGGAGAGCGTTAAGAAACACAAACGGCTGGAT  
 141 T R I V G L D Q Y L E S V K K H K R L D  
 481 GTGTGCCGCGCTAAAATGGGCTATATGCTGCAGTGA  
 161 V C R A K M G Y M L Q \*



Figure 14

**Translation of SEQUL130: HCK-5 (pUL130)**

```

1      ATGCTACGGCTTCTGCTTCGTCACCACTTTCACTGCCTGCTTCTGTGCGCGGTTTGGGCA
1      M L R L L L R H H F H C L L L C A V W A

61     ACGCCCTGTCTGGCGTCTCCGTGGTTACGCTAACGGCGAACCAGAATCCGTCCCCGCCA
21     T P C L A S P W F T L T A N Q N P S P P

121    TGGTCTAAACTGACGTATCCCAAACCGCATGACGCGGCGACGTTTACTGTCTTTTCTC
41     W S K L T Y P K P H D A A T F Y C P F L

181    TATCCCTCGCCCCACGGTCCCCCTCGCAATTCCCGGGGTTCAGCGGGTATCAACGGGT
61     Y P S P P R S P S Q F P G F Q R V S T G

241    CCCGAGTGTGCAACGAGACCCTGTATCTGCTGTACAACGGGAAGGCCAGACCTTGGTG
81     P E C R N E T L Y L L Y N R E G Q T L V

301    GAGAGAAGCTCCACCTGGGTGAAAAAGGTGATCTGGTATCTGAGCGGTGCAATCAGACC
101    E R S S T W V K K V I W Y L S G R N Q T

361    ATCCTCCAACGGATGCCCCGAACGGCTTCGAAACCGAGCGACGGAAACGTGCAGATCAGC
121    I L Q R M P R T A S K P S D G N V Q I S

421    GTGGAAGACGCCAAGATTTTTGGAGCGCACATGGTGCCCAAGCAGACCAAGCTGCTACGT
141    V E D A K I F G A H M V P K Q T K L L R

481    TTCGTCGTCAACGATGGCACACGTTATCAGATGTGTGTGATGAAACTGGAGAGCTGGGCC
161    F V V N D G T R Y Q M C V M K L E S W A

541    CACGTCTTCCGGGACTACAGCGTGTCTTTTCAGGTGCGATTGACGTTACCGAGGCCAAT
181    H V F R D Y S V S F Q V R L T F T E A N

601    AACCAGACTTACACCTTCTGCACCCATCCCAATCTCATCGTTTGA
201    N Q T Y T F C T H P N L I V *

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